WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Wednesday, February 02, 2005

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ	
☐	L1	tamura-T$.in.	8783
☐	L2	oto-N$.in. or suzuki-N$.in. or mizuno-K$.in. L1	12951
☐	L3	oto-N$.in. or suzuki-N$.in. or mizuno-K$.in.	17323
☐	L4	yamamoto-N$.in. or suzuki-N$.in. or mizuno-K$.in.	24242
☐	L5	(L1 or L4) and (biochip or array)	682
☐	L6	(L1 or L4) and (biochip or microarray or array)	697
☐	L7	L6 and hybridiz$	62
☐	L8	L7 and biopolymer	20
☐	L9	L8 and visual$	7
☐	L10	probe similarity score	0
☐	L11	similarity score	1108
☐	L12	biochip or microarray	16282
☐	L13	L12 same bipolymer	1
☐	L14	L11 and L12	62
☐	L15	L14 and biopolymer	13
☐	L16	L15 and (imag$ and visual$)	9
☐	L17	L16 and hybridiz$	9
☐	L18	L12 and biopolymer	1568
☐	L19	L18 and hybridiz$	1399
☐	L20	L19 and (similar$ scor$ or percent homology or percent identity or sequence identity)	491
☐	L21	L20 and (display$ and imag$ and visual$)	295
☐	L22	L21 and (different same color)	26
☐	L23	L22 and (different same (valu$ or depth))	20
☐	L24	L23 and spot imag$	1
☐	L25	L23 and statistic$	20
☐	L26	L25 and matrix	18
☐	L27	L26 and (hybridization level or hybridization profile)	1
☐	L28	L25 and storage unit	1
☐	L29	L25 and (data near storage)	7

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     FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT, CAPLUS,
     BIOTECHNO' ENTERED AT 16:01:12 ON 02 FEB 2005
L1         18530 S (IDENTITY OR SIMILAR? OR HOMOLOG?) (10A) (PROBE OR OLIGOMER O
L2           261 S L1 AND (BLAST OR SIMOTH-WATERSON OR ALGORITHM)
L3             5 S L2 AND (VISUAL? OR GRAPH?)
L4           104 S L2 AND (HYBRIDIZ?)
L5            11 S L4 AND (DISPLAY OR VISUAL? OR GRAPH? OR REPRESENTATION OR CO

=> s biochip same (probe or oliomer or biopolymer or oligonucleotide)
MISSING OPERATOR 'SAME (PROBE'
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s biochip (6a) (probe# or oliomer# or biopolymer# or oligonucleotide#)
L6           426 BIOCHIP (6A) (PROBE# OR OLIOMER# OR BIOPOLYMER# OR OLIGONUCLEOTI
                 DE#)

=> s l6 an(Blast or Smith-Waterson or algorithm)
<------User Break------>
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     (FILE 'HOME' ENTERED AT 16:00:23 ON 02 FEB 2005)

     FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT, CAPLUS,
     BIOTECHNO' ENTERED AT 16:01:12 ON 02 FEB 2005
L1         18530 S (IDENTITY OR SIMILAR? OR HOMOLOG?) (10A) (PROBE OR OLIGOMER O
L2           261 S L1 AND (BLAST OR SIMOTH-WATERSON OR ALGORITHM)
L3             5 S L2 AND (VISUAL? OR GRAPH?)
L4           104 S L2 AND (HYBRIDIZ?)
L5            11 S L4 AND (DISPLAY OR VISUAL? OR GRAPH? OR REPRESENTATION OR CO
L6           426 S BIOCHIP (6A) (PROBE# OR OLIOMER# OR BIOPOLYMER# OR OLIGONUCLE

     FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT, CAPLUS,
     BIOTECHNO' ENTERED AT 16:27:42 ON 02 FEB 2005
L7        6955782 S (IDENTITY OR SIMILAR? OR HOMOLOG? OR SIMILARITY SCORE)
L8          18530 S L1 (10A) (PROBE OR OLIGOMER OR OLIGONUCLEOTIDE OR BIOPOLYMER)
L9            261 S L8 AND (BLAST OR SMITH-WATERSON OR ALGORITHM)
L10            39 S L9 AND (BIOCHIP OR ARRAY OR CHIP OR MICROARRAY OR HYBRIDIZAT
L11            26 DUP REM L10 (13 DUPLICATES REMOVED)

     FILE 'STNGUIDE' ENTERED AT 16:40:03 ON 02 FEB 2005

     FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT, CAPLUS,
     BIOTECHNO' ENTERED AT 16:45:11 ON 02 FEB 2005
L12             0 S PROBE VERSUS PROBE
L13          2142 S PROBE (5A) COMPARISON
L14            31 S L13 AND ALGORITHM
L15            10 S L14 AND (IDENTITY OR SIMILAR? OR HOMOLOG? OR SIMILARITY SCOR
L16        510538 S (BLAST OR SMITH-WATERSON OR ALGORITHM)
L17         17831 S L16 AND (ARRAY OR MICROARRAY OR BIOCHIP OR CHIP OR HYBRIDIZA
L18            33 S L17 AND (LEVEL (3A) HYBRIDIZ?)
L19          3139 S L17 AND (DISPLAY? OR GRAPH? OR CLUSTER?)
L20             3 S L18 AND (CLUSTER?)

     FILE 'STNGUIDE' ENTERED AT 16:55:13 ON 02 FEB 2005

=>
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123:331092

TITLE: DNA sequence recognition by hybridization to short oligomers

AUTHOR(S): Milosavljevic, Aleksandar

CORPORATE SOURCE: Center Biol. Biotechnology, Argonne National Lab., Argonne, IL, 60439-4833, USA

SOURCE: Journal of Computational Biology (1995), 2(2), 355-70
CODEN: JCOBEM; ISSN: 1066-5277

PUBLISHER: Liebert

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A format 1 technol. for performing massive hybridization expts. has been developed as part of the sequencing by hybridization (SBH) project. Arrays of tens of thousands of clones are interrogated with short oligomer probes to determine sets of oligomers that are present in individual clones. SBH requires highly discriminative hybridizations with a large number of probes. One of the main uses of a reconstructed DNA sequence is in a similarity search against databases of known DNA. The authors argue that sequence reconstruction, even partial, should not be performed for this particular purpose; the authors provide and information-theoretic proof that the **oligomer** lists obtained from hybridization expts. should be used directly for **similarity** searches. The authors propose a similarity search method that takes full advantage of the subword structure of pos. identified oligomers within a clone. The method tolerates error in hybridization expts., requires fewer probes than necessary for sequencing, and is computationally efficient. To enable direct sequence recognition, the authors apply the recently developed method of sequence comparison that is based on minimal length encoding and algorithmic mutual information. The method has been tested on both real and simulated data and has led to a correct identification of clones based on hybridizations with 109 short oligomer probes. The method is applicable to hybridization data that comes from both format 1 and format 2 (sequencing **chip**) hybridization expts. The sequence recognition method can provide targeting information for large-scale DNA sequencing by gel-based methods or by hybridization.

Computers & Chemistry
Volume 23, Issues 3-4 , 15 June 1999, Pages 251-262

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An **algorithm** for the assembly of robust physical maps based on a combination of multi-**level** **hybridization** data and fingerprinting data.

AUTHOR: Sasinowska H; Sasinowski M
CORPORATE SOURCE: Department of Mathematical Sciences, Clemson University, Clemson, SC 29634, USA.. heather@math.clemson.edu
SOURCE: Computers & chemistry, (1999 Jun 15) 23 (3-4) 251-62.
Journal code: 7607706. ISSN: 0097-8485.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200001
ENTRY DATE: Entered STN: 20000114
Last Updated on STN: 20000114
Entered Medline: 20000104

AB We have developed an **algorithm** which combines data obtained from restriction digestion experiments and **hybridization** experiments to construct robust physical maps of whole chromosomes. The **algorithm** has been incorporated into a program which accepts **hybridization** data consisting of an unordered **hybridization** matrix and fingerprinting data containing band coordinates for each clone. The combined data is used to produce a non-redundant, ordered matrix which can be further reduced to represent a minimum tile coverage of the chromosome. In addition, the method also takes into account multi-**level** **hybridization** events which allows for an improved treatment of the **hybridization** data. The program is evaluated against several other contig building programs using simulated and real data sets. Finally, it is applied to construct a physical map of the 4.1 Mb genome of Ochrobactrum anthropi based on 1387 clones and 70 probes, as well as 624 fingerprints.

=> FIL STNGUIDE
COST IN U.S. DOLLARS

	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	99.10	331.93

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-1.46	-8.76

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FILE CONTAINS CURRENT INFORMATION.
LAST RELOADED: Jan 28, 2005 (20050128/UP).

=>

☐	L30	L25 and hybridization	20
☐	L31	((biopolymer or probe) near (biochip or microarry))	188
☐	L32	L31 and ((display$ or visual$) same hybridiz$)	14
☐	L33	(display$ or visual$) same (percent identity or percent homology or sequence identity or sequence similarity or similarity score)	3047
☐	L34	L33 same (hybridization)	105
☐	L35	L34 and (graphic$)	11
☐	L36	L33 and (different near color)	57
☐	L37	L36 and (image)	36
☐	L38	L31 and L33	23
☐	L39	(display$ or visual$)near(percent identity or percent homology or sequence identity or sequence similarity or similarity score)	130
☐	L40	L39 and hybridiz$	101
☐	L41	L40 and (biochip or microarray)	21
☐	L42	L41 and (biopolymer or probe)	21
☐	L43	L39 and (biochip or microarray)	21
☐	L44	L33 and (biochip or microarray)	467
☐	L45	L44 and hybridization	436
☐	L46	L45 and ((Imag$ or matrix or graphic$) same (different near color))	1
☐	L47	L45 and ((Imag$ or matrix or graphic$) and (different near color))	6
☐	L48	BLAST same (imag$ or graphic$ or visual$)	4304
☐	L49	L48 same (biochip or micrarray)	5
☐	L50	6188783.pn. or 5812272.pn. or 6471916.pn. or 6284465.pn.	8
☐	L51	6349144.pn. or 4852183.pn. or 6306643.pn. or 6228575.pn.	8
☐	L52	(identity or similarity) near score	2210
☐	L53	L52 same probe$	12
☐	L54	L52 and l48	22
☐	L55	L54 and prob$	21
☐	L56	L52 and (BLAST or smith-waterson or algorithm)	1790
☐	L57	L52 same (probe or oligonucleotide or biopolymer or oligomer)	18

END OF SEARCH HISTORY